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Reviewer: Anne Corrigan

Timestamp: Thu Oct 18 15:52:58 EDT 2007

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Application No: 10784528 Version No: 2.0

Input Set:

Output Set:

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Finished: 2007-10-02 19:27:39.130  
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 713 ms  
Total Warnings: 2  
Total Errors: 0  
No. of SeqIDs Defined: 10  
Actual SeqID Count: 10

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)

# SEQUENCE LISTING

<110> BROWN, ARTHUR M.  
WIBLE, BARBARA A.

<120> METHODS OF INDUCING APOPTOSIS IN HYPERPROLIFERATION  
CELLS

<130> 22884/04085

<140> 10784528

<141> 2004-02-23

<150> 10/000,778

<151> 2001-10-31

<160> 10

<170> PatentIn Ver. 3.3

<210> 1

<211> 1725

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1722)

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ggg ccc tct gat ctc tcc ctt ctc tct ttg ccc cct ggc acc tct cct	96
Gly Pro Ser Asp Leu Ser Leu Leu Ser Leu Pro Pro Gly Thr Ser Pro	
20 25 30	

gta ggc tcc cct ggt cct cta gct ccc att ccc cca acg ctg ttg gcc	144
Val Gly Ser Pro Gly Pro Leu Ala Pro Ile Pro Pro Thr Leu Leu Ala	
35 40 45	

cct ggc acc ctg ctg ggc ccc aag cgt gag gtg gac atg cac ccc cct	192
Pro Gly Thr Leu Leu Gly Pro Lys Arg Glu Val Asp Met His Pro Pro	
50 55 60	

ctg ccc cag cct gtg cac cct gat gtc acc atg aaa cca ttg ccc ttc	240
Leu Pro Gln Pro Val His Pro Asp Val Thr Met Lys Pro Leu Pro Phe	
65 70 75 80	

tat gaa gtc tat ggg gag ctc atc cgg ccc acc acc ctt gca tcc act	288
Tyr Glu Val Tyr Gly Glu Leu Ile Arg Pro Thr Thr Leu Ala Ser Thr	
85 90 95	

tct agc cag cgg ttt gag gaa gcg cac ttt acc ttt gcc ctc aca ccc	336
Ser Ser Gln Arg Phe Glu Glu Ala His Phe Thr Phe Ala Leu Thr Pro	

100	105	110	
cag caa gtg cag cag att ctt aca tcc aga gag gtt ctg cca gga gcc			384
Gln Gln Val Gln Gln Ile Leu Thr Ser Arg Glu Val Leu Pro Gly Ala			
115	120	125	
aaa tgt gat tat acc ata cag gtg cag cta agg ttc tgt ctc tgt gag			432
Lys Cys Asp Tyr Thr Ile Gln Val Gln Leu Arg Phe Cys Leu Cys Glu			
130	135	140	
acc agc tgc ccc cag gaa gat tat ttt ccc ccc aac ctc ttt gtc aag			480
Thr Ser Cys Pro Gln Glu Asp Tyr Phe Pro Pro Asn Leu Phe Val Lys			
145	150	155	160
gtt aat ggg aaa ctg tgc ccc ctg ccg ggt tac ctt ccc cca acc aag			528
Val Asn Gly Lys Leu Cys Pro Leu Pro Gly Tyr Leu Pro Pro Thr Lys			
165	170	175	
aat ggg gcc gag ccc aag agg ccc agc cgc ccc atc aac atc aca ccc			576
Asn Gly Ala Glu Pro Lys Arg Pro Ser Arg Pro Ile Asn Ile Thr Pro			
180	185	190	
ctg gct cga ctc tca gcc act gtt ccc aac acc att gtg gtc aat tgg			624
Leu Ala Arg Leu Ser Ala Thr Val Pro Asn Thr Ile Val Val Asn Trp			
195	200	205	
tca tct gag ttc gga cgg aat tac tcc ttg tct gtg tac ctg gtg agg			672
Ser Ser Glu Phe Gly Arg Asn Tyr Ser Leu Ser Val Tyr Leu Val Arg			
210	215	220	
cag ttg act gca gga acc ctt cta caa aaa ctc aga gca aag ggt atc			720
Gln Leu Thr Ala Gly Thr Leu Leu Gln Lys Leu Arg Ala Lys Gly Ile			
225	230	235	240
cgg aac cca gac cac tcg cgg gca ctg atc aag gag aaa ttg act gct			768
Arg Asn Pro Asp His Ser Arg Ala Leu Ile Lys Glu Lys Leu Thr Ala			
245	250	255	
gac cct gac agt gag gtg gcc act aca agt ctc cgg gtg tca ctc atg			816
Asp Pro Asp Ser Glu Val Ala Thr Thr Ser Leu Arg Val Ser Leu Met			
260	265	270	
tgc ccg cta ggg aag atg cgc ctg act gtc cct tgt cgt gcc ctc acc			864
Cys Pro Leu Gly Lys Met Arg Leu Thr Val Pro Cys Arg Ala Leu Thr			
275	280	285	
tgt gcc cac ctg cag agc ttc gat gct gcc ctt tat cta cag atg aat			912
Cys Ala His Leu Gln Ser Phe Asp Ala Ala Leu Tyr Leu Gln Met Asn			
290	295	300	
gag aag aag cct aca tgg aca tgt cct gtg tgt gac aag aag gct ccc			960
Glu Lys Lys Pro Thr Trp Thr Cys Pro Val Cys Asp Lys Lys Ala Pro			
305	310	315	320
tat gaa tct ctt atc att gat ggt tta ttt atg gag att ctt agt tcc			1008
Tyr Glu Ser Leu Ile Ile Asp Gly Leu Phe Met Glu Ile Leu Ser Ser			
325	330	335	

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Cys Ser Asp Cys Asp Glu Ile Gln Phe Met Glu Asp Gly Ser Trp Cys	
340 345 350	
cca atg aaa ccc aag aag gag gca tct gag gtt tgc ccc ccg cca ggg	1104
Pro Met Lys Pro Lys Lys Glu Ala Ser Glu Val Cys Pro Pro Pro Gly	
355 360 365	
tat ggg ctg gat ggc ctc cag tac agc cca gtc cag ggg gga gat cca	1152
Tyr Gly Leu Asp Gly Leu Gln Tyr Ser Pro Val Gln Gly Gly Asp Pro	
370 375 380	
tca gag aat aag aag aag gtc gaa gtt att gac ttg aca ata gaa agc	1200
Ser Glu Asn Lys Lys Lys Val Glu Val Ile Asp Leu Thr Ile Glu Ser	
385 390 395 400	
tca tca gat gag gag gat ctg ccc cct acc aag aag cac tgt tct gtc	1248
Ser Ser Asp Glu Glu Asp Leu Pro Pro Thr Lys Lys His Cys Ser Val	
405 410 415	
acc tca gct gcc atc ccg gcc cta cct gga agc aaa gga gtc ctg aca	1296
Thr Ser Ala Ala Ile Pro Ala Leu Pro Gly Ser Lys Gly Val Leu Thr	
420 425 430	
tct ggc cac cag cca tcc tcg gtg cta agg agc cct gct atg ggc acg	1344
Ser Gly His Gln Pro Ser Ser Val Leu Arg Ser Pro Ala Met Gly Thr	
435 440 445	
ttg ggt ggg gat ttc ctg tcc agt ctc cca cta cat gag tac cca cct	1392
Leu Gly Gly Asp Phe Leu Ser Ser Leu Pro Leu His Glu Tyr Pro Pro	
450 455 460	
gcc ttc cca ctg gga gcc gac atc caa ggt tta gat tta ttt tca ttt	1440
Ala Phe Pro Leu Gly Ala Asp Ile Gln Gly Leu Asp Leu Phe Ser Phe	
465 470 475 480	
ctt cag aca gag agt cag cac tat ggc ccc tct gtc atc acc tca cta	1488
Leu Gln Thr Glu Ser Gln His Tyr Gly Pro Ser Val Ile Thr Ser Leu	
485 490 495	
gat gaa cag gat gcc ctt ggc cac ttc ttc cag tac cga ggg acc cct	1536
Asp Glu Gln Asp Ala Leu Gly His Phe Phe Gln Tyr Arg Gly Thr Pro	
500 505 510	
tct cac ttt ctg ggc cca ctg gcc ccc acg ctg ggg agc tcc cac tgc	1584
Ser His Phe Leu Gly Pro Leu Ala Pro Thr Leu Gly Ser Ser His Cys	
515 520 525	
agc gcc act ccg gcg ccc cct cct ggc cgt gtc agc agc att gtg gcc	1632
Ser Ala Thr Pro Ala Pro Pro Pro Gly Arg Val Ser Ser Ile Val Ala	
530 535 540	
cct ggg ggg gcc ttg agg gag ggg cat gga gga ccc ctg ccc tca ggt	1680
Pro Gly Gly Ala Leu Arg Glu Gly His Gly Gly Pro Leu Pro Ser Gly	
545 550 555 560	

ccc tct ttg act ggc tgt cgg tca gac atc att tcc ctg gac tga 1725  
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565 570

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<212> PRT  
<213> Homo sapiens

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Gly Pro Ser Asp Leu Ser Leu Leu Ser Leu Pro Pro Gly Thr Ser Pro  
20 25 30

Val Gly Ser Pro Gly Pro Leu Ala Pro Ile Pro Pro Thr Leu Leu Ala  
35 40 45

Pro Gly Thr Leu Leu Gly Pro Lys Arg Glu Val Asp Met His Pro Pro  
50 55 60

Leu Pro Gln Pro Val His Pro Asp Val Thr Met Lys Pro Leu Pro Phe  
65 70 75 80

Tyr Glu Val Tyr Gly Glu Leu Ile Arg Pro Thr Thr Leu Ala Ser Thr  
85 90 95

Ser Ser Gln Arg Phe Glu Glu Ala His Phe Thr Phe Ala Leu Thr Pro  
100 105 110

Gln Gln Val Gln Gln Ile Leu Thr Ser Arg Glu Val Leu Pro Gly Ala  
115 120 125

Lys Cys Asp Tyr Thr Ile Gln Val Gln Leu Arg Phe Cys Leu Cys Glu  
130 135 140

Thr Ser Cys Pro Gln Glu Asp Tyr Phe Pro Pro Asn Leu Phe Val Lys  
145 150 155 160

Val Asn Gly Lys Leu Cys Pro Leu Pro Gly Tyr Leu Pro Pro Thr Lys  
165 170 175

Asn Gly Ala Glu Pro Lys Arg Pro Ser Arg Pro Ile Asn Ile Thr Pro  
180 185 190

Leu Ala Arg Leu Ser Ala Thr Val Pro Asn Thr Ile Val Val Asn Trp  
195 200 205

Ser Ser Glu Phe Gly Arg Asn Tyr Ser Leu Ser Val Tyr Leu Val Arg  
210 215 220

Gln Leu Thr Ala Gly Thr Leu Leu Gln Lys Leu Arg Ala Lys Gly Ile  
225 230 235 240

Arg Asn Pro Asp His Ser Arg Ala Leu Ile Lys Glu Lys Leu Thr Ala

245	250	255
Asp Pro Asp Ser Glu Val Ala Thr Thr Ser Leu Arg Val Ser Leu Met		
260	265	270
Cys Pro Leu Gly Lys Met Arg Leu Thr Val Pro Cys Arg Ala Leu Thr		
275	280	285
Cys Ala His Leu Gln Ser Phe Asp Ala Ala Leu Tyr Leu Gln Met Asn		
290	295	300
Glu Lys Lys Pro Thr Trp Thr Cys Pro Val Cys Asp Lys Lys Ala Pro		
305	310	315
Tyr Glu Ser Leu Ile Ile Asp Gly Leu Phe Met Glu Ile Leu Ser Ser		
325	330	335
Cys Ser Asp Cys Asp Glu Ile Gln Phe Met Glu Asp Gly Ser Trp Cys		
340	345	350
Pro Met Lys Pro Lys Lys Glu Ala Ser Glu Val Cys Pro Pro Pro Gly		
355	360	365
Tyr Gly Leu Asp Gly Leu Gln Tyr Ser Pro Val Gln Gly Gly Asp Pro		
370	375	380
Ser Glu Asn Lys Lys Lys Val Glu Val Ile Asp Leu Thr Ile Glu Ser		
385	390	395
Ser Ser Asp Glu Glu Asp Leu Pro Pro Thr Lys Lys His Cys Ser Val		
405	410	415
Thr Ser Ala Ala Ile Pro Ala Leu Pro Gly Ser Lys Gly Val Leu Thr		
420	425	430
Ser Gly His Gln Pro Ser Ser Val Leu Arg Ser Pro Ala Met Gly Thr		
435	440	445
Leu Gly Gly Asp Phe Leu Ser Ser Leu Pro Leu His Glu Tyr Pro Pro		
450	455	460
Ala Phe Pro Leu Gly Ala Asp Ile Gln Gly Leu Asp Leu Phe Ser Phe		
465	470	475
Leu Gln Thr Glu Ser Gln His Tyr Gly Pro Ser Val Ile Thr Ser Leu		
485	490	495
Asp Glu Gln Asp Ala Leu Gly His Phe Phe Gln Tyr Arg Gly Thr Pro		
500	505	510
Ser His Phe Leu Gly Pro Leu Ala Pro Thr Leu Gly Ser Ser His Cys		
515	520	525
Ser Ala Thr Pro Ala Pro Pro Pro Gly Arg Val Ser Ser Ile Val Ala		
530	535	540
Pro Gly Gly Ala Leu Arg Glu Gly His Gly Gly Pro Leu Pro Ser Gly		

545 550 555 560

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<211> 28  
<212> PRT  
<213> Artificial Sequence

<220>  
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Thr Leu Leu Gly Pro Lys Arg Glu Val Asp Met His  
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<210> 4  
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<220>  
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peptide

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<211> 650  
<212> PRT  
<213> Homo sapiens

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1 5 10 15

Ser Glu Leu Gln Val Leu Leu Gly Tyr Ala Gly Arg Asn Lys His Gly  
20 25 30

Arg Lys His Glu Leu Leu Thr Lys Ala Leu His Leu Leu Lys Ala Gly  
35 40 45

Cys Ser Pro Ala Val Gln Met Lys Ile Lys Glu Leu Tyr Arg Arg Arg  
50 55 60

Phe Pro Gln Lys Ile Met Thr Pro Ala Asp Leu Ser Ile Pro Asn Val



65		70		75		80
His Ser Ser Pro Met Pro Ala Thr Leu Ser Pro Ser Thr Ile Pro Gln						
	85		90		95	
Leu Thr Tyr Asp Gly His Pro Ala Ser Ser Pro Leu Leu Pro Val Ser						
	100		105		110	
Leu Leu Gly Pro Lys His Lys Leu Glu Leu Pro His Leu Thr Ser Ala						
	115		120		125	
Leu His Pro Val His Pro Asp Ile Lys Leu Gln Lys Leu Pro Phe Tyr						
	130		135		140	
Asp Leu Leu Asp Glu Leu Ile Lys Pro Thr Ser Leu Ala Ser Asp Asn						
	145		150		155	160
Ser Gln Arg Phe Arg Glu Thr Cys Phe Ala Phe Ala Leu Thr Pro Gln						
	165		170		175	
Gln Val Gln Gln Ile Ser Ser Ser Met Asp Ile Ser Gly Thr Lys Cys						
	180		185		190	
Asp Phe Thr Val Gln Val Gln Leu Arg Phe Cys Leu Ser Glu Thr Ser						
	195		200		205	
Cys Pro Gln Glu Asp His Phe Pro Pro Asn Leu Cys Val Lys Val Asn						
	210		215		220	
Thr Lys Pro Cys Ser Leu Pro Gly Tyr Leu Pro Pro Thr Lys Asn Gly						
	225		230		235	240
Val Glu Pro Lys Arg Pro Ser Arg Pro Ile Asn Ile Thr Ser Leu Val						
	245		250		255	
Arg Leu Ser Thr Thr Val Pro Asn Thr Met Cys Ser Trp Thr Ala Glu						
	260		265		270	
Ile Gly Arg Asn Tyr Ser Met Ala Val Tyr Leu Val Lys Gln Leu Ser						
	275		280		285	
Ser Thr Val Leu Leu Gln Arg Leu Arg Ala Lys Gly Ile Arg Asn Pro						
	290		295		300	
Asp His Ser Arg Ala Leu Ile Lys Glu Lys Leu Thr Ala Asp Pro Asp						
	305		310		315	320
Ser Glu Ile Ala Thr Thr Ser Leu Arg Val Ser Leu Leu Cys Pro Leu						
	325		330		335	
Gly Lys Met Arg Leu Thr Ile Pro Cys Arg Ala Leu Thr Cys Ser His						
	340		345		350	
Leu Gln Cys Phe Asp Ala Thr Leu Tyr Ile Gln Met Asn Glu Lys Lys						
	355		360		365	
Pro Thr Trp Val Cys Pro Val Cys Asp Lys Lys Ala Pro Tyr Glu His						

370		375		380	
Leu Ile Ile Asp Gly	Leu Phe Met Glu Ile	Leu Lys Tyr Cys Thr Asp			
385	390	395		400	
Cys Asp Glu Ile Gln	Phe Lys Glu Asp Gly	Thr Trp Ala Pro Met Arg			
	405	410		415	
Ser Lys Lys Glu Val	Gln Glu Val Ser Ala	Ser Tyr Asn Gly Val Asp			
	420	425		430	
Gly Cys Leu Ser Ser	Thr Leu Glu His Gln	Val Ala Ser His His Gln			
	435	440		445	
Ser Ser Asn Lys Asn	Lys Lys Val Glu Val	Ile Asp Leu Thr Ile Asp			
	450	455		460	
Ser Ser Ser Asp Glu	Glu Glu Glu Glu Pro	Ser Ala Lys Arg Thr Cys			
465	470	475		480	
Pro Ser Leu Ser Pro	Thr Ser Pro Leu Asn	Asn Lys Gly Ile Leu Ser			
	485	490		495	
Leu Pro His Gln Ala	Ser Pro Val Ser Arg	Thr Pro Ser Leu Pro Ala			
	500				